

From taxonomic deflation to newly detected cryptic species: Hidden diversity in a widespread African squeaker catfish

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Supplementary data

Table S1. Sequences of *cox1*, *cytb* and *RAG2* for *Synodontis* spp. from the Nile and Turkana deposited in GenBank, including detailed information on localities. Data provided in separate file.

Table S2. List of GenBank *cox1*, *cytb* and *RAG2* *Synodontis* spp. sequences used in phylogenetic and haplotype analyses. Data provided in separate file. The data obtained from the same sample are highlighted by bold.

Table S3. Results of chi-square test for spatial distribution of *S. schall*, *S. frontosus* and intermediate morphotypes.

obs.	El Molo	Kalokol	Todonyang	totals(marginals)	
1	35	19	32	86	
2	16	11	31	58	
3	7	0	14	21	
	58	30	77	165	

obs. frekv.	El Molo	Kalokol	Todonyang	null (expected)	
1	0,603	0,63	0,415	0,52	
2	0,276	0,36	0,402	0,35	
3	0,121	0	0,181	0,13	

expected counts	El Molo	Kalokol	Todonyang		
1	30,23	15,63	40,13		
2	20,38	10,54	27,06		
3	7,38	3,81	9,8		

	El Molo	Kalokol	Todonyang		
χ^2	0,753	0,723	1,648		
	0,944	0,019	0,571		
	0,019	3,818	1,8		
	1,716	4,561	4,019	10,297	

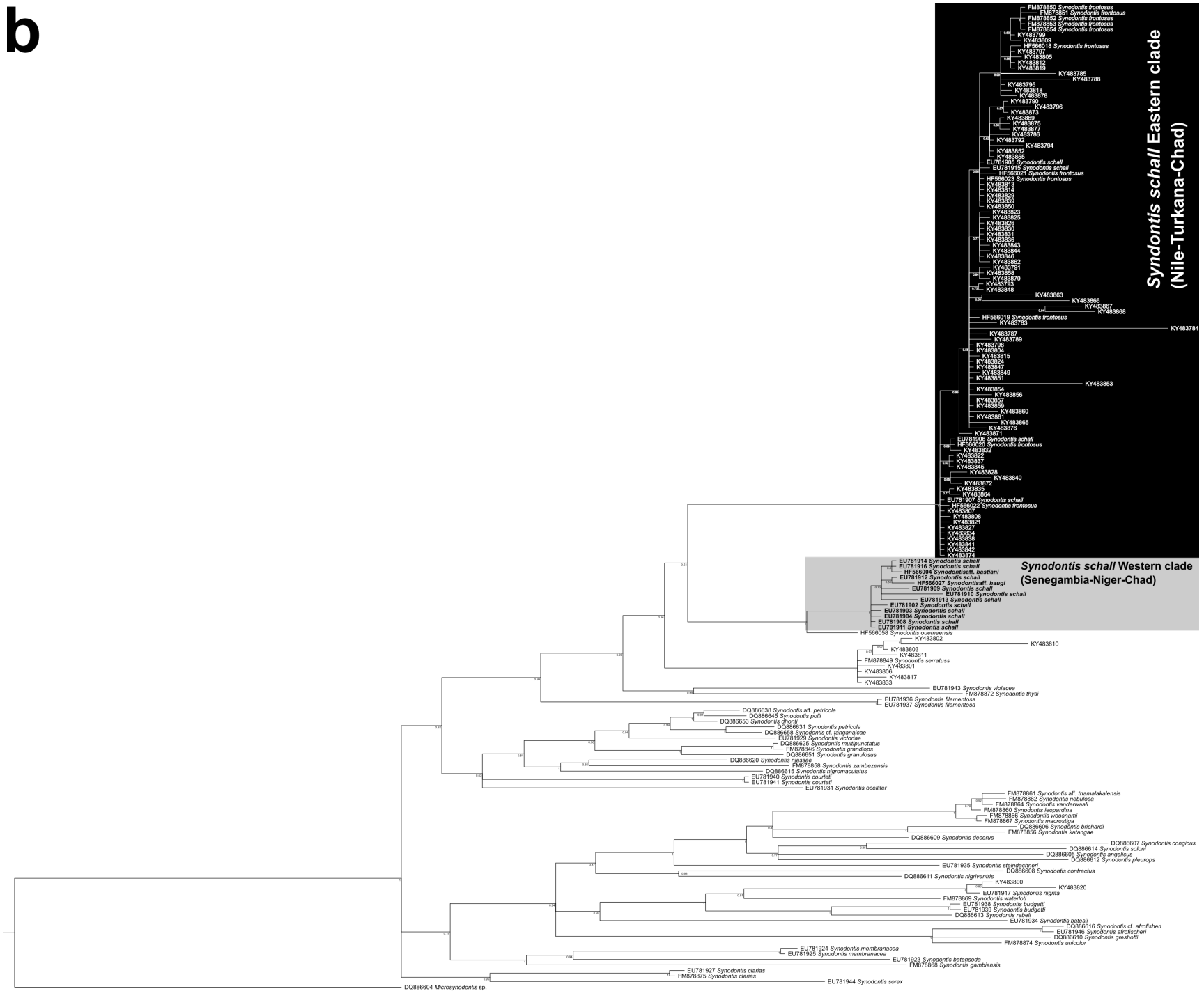
P(=0,05; df=4)	9,488				
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Table S4. Results of population genetics analyses between *S. schall*-like and *S. frontosus*-like morphotype from Eastern Africa (the Nile and Turkana) obtained for this study. The genetic differentiation between the sequences from three Turkana localities was tested by the *Snn* test and showed that the saline locality differs from the freshwater and medium part.

	Haplotype diversity			
	<i>coxI</i>	<i>cytb</i>		
<i>S. schall</i> -like	0.36	0.97		
<i>S. frontosus</i> -like	0.65	0.97		
	Fst			
	<i>coxI</i>	<i>cytb</i>		
<i>S. schall</i> -like x <i>S. frontosus</i> -like	0.08	0.04		
	Genetic differentiation			
	<i>coxI</i>		<i>cytb</i>	
	<i>Chi-square</i>	<i>P</i>	<i>Chi-square</i>	<i>P</i>
<i>S. schall</i> -like x <i>S. frontosus</i> -like	34.487	0.0029	51.934	0.1922
	Genetic distance			
	<i>coxI</i>	<i>cytb</i>		
<i>S. schall</i> -like	0 - 0.88 %	0 - 1.75%		
<i>S. frontosus</i> -like	0 - 1.06%	0 - 1.95%		
<i>S. schall</i> -like x <i>S. frontosus</i> -like	0 - 1.06%	0 - 2.06%		

Turkana localities							
	Haplotype diversity						
	<i>coxI</i>	<i>cytb</i>					
Medium salinity	0.38	1.00					
Freshwater	0.40	0.98					
Saline water	0.67	0.93					
	Fst						
	<i>coxI</i>				<i>cytb</i>		
	Medium salinity	Freshwater	Saline water		Medium salinity	Freshwater	Saline water
Medium salinity	x			Medium salinity	x		
Freshwater	0.00585	x		Freshwater	0.063	x	
Saline water	0.18779	0.17877	x	Saline water	0.047	0.010	x
	Snn test						
	<i>coxI</i>	<i>cytb</i>					
<i>Snn</i>	0.68	0.543					
<i>P-value</i>	0.018	0.094*					
* not significant P-value							

b



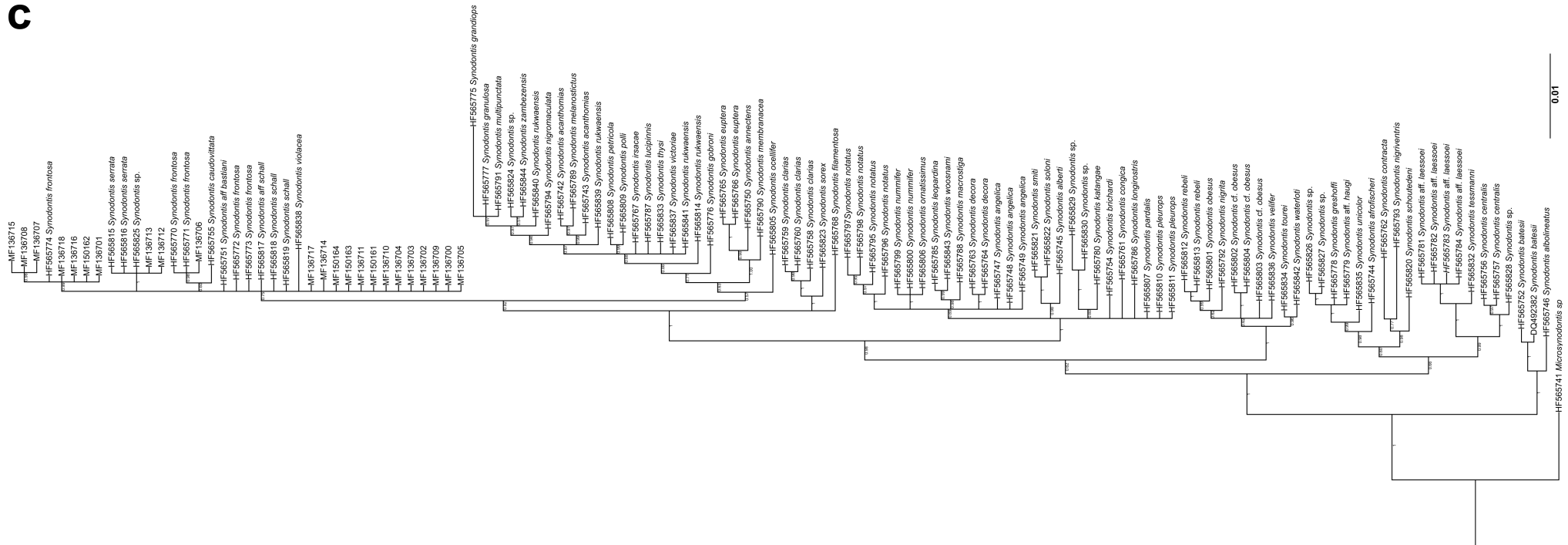
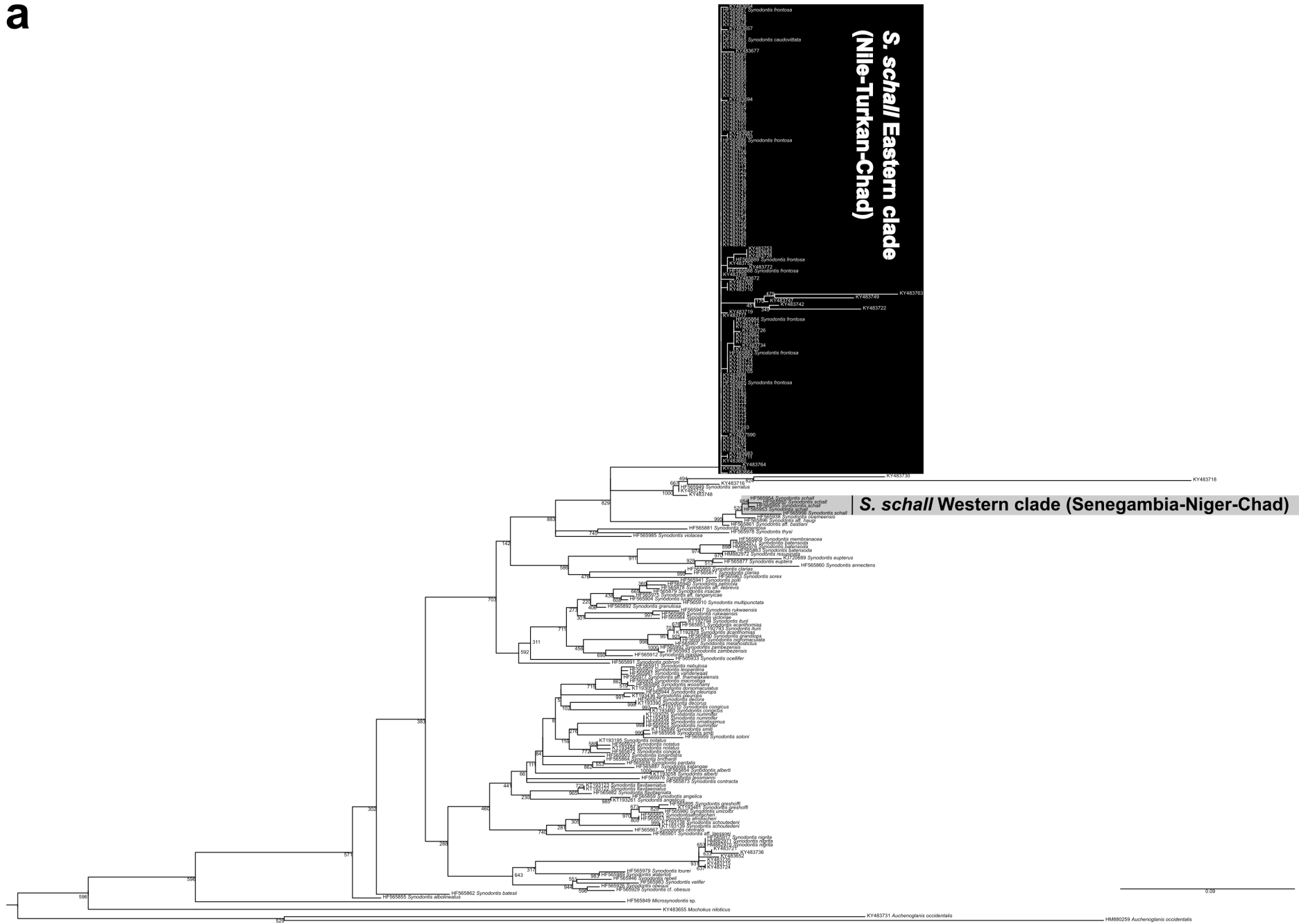
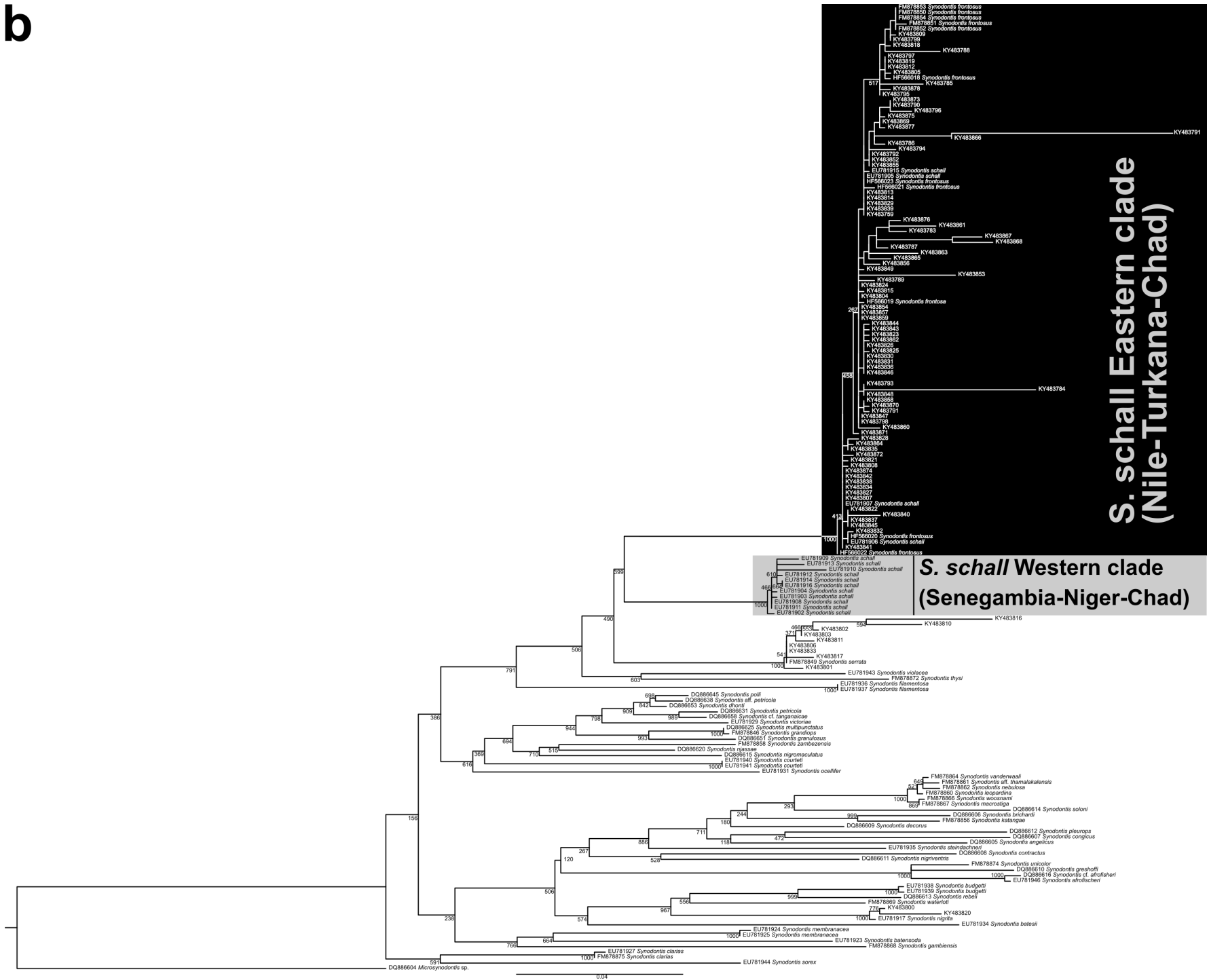
C

Figure S1. Phylogenetic trees for *cox1* a), *cytb* b) and *RAG2* c) as revealed by BI analyses, showing detailed branching with posterior probabilities as branch supports. Final trees were created by software MrBayes. Sequence data of *S. schall* Eastern clade obtained within the scope of this study are presented with GenBank numbers. Data provided in separate file (see Tab. S2).

a



b



C

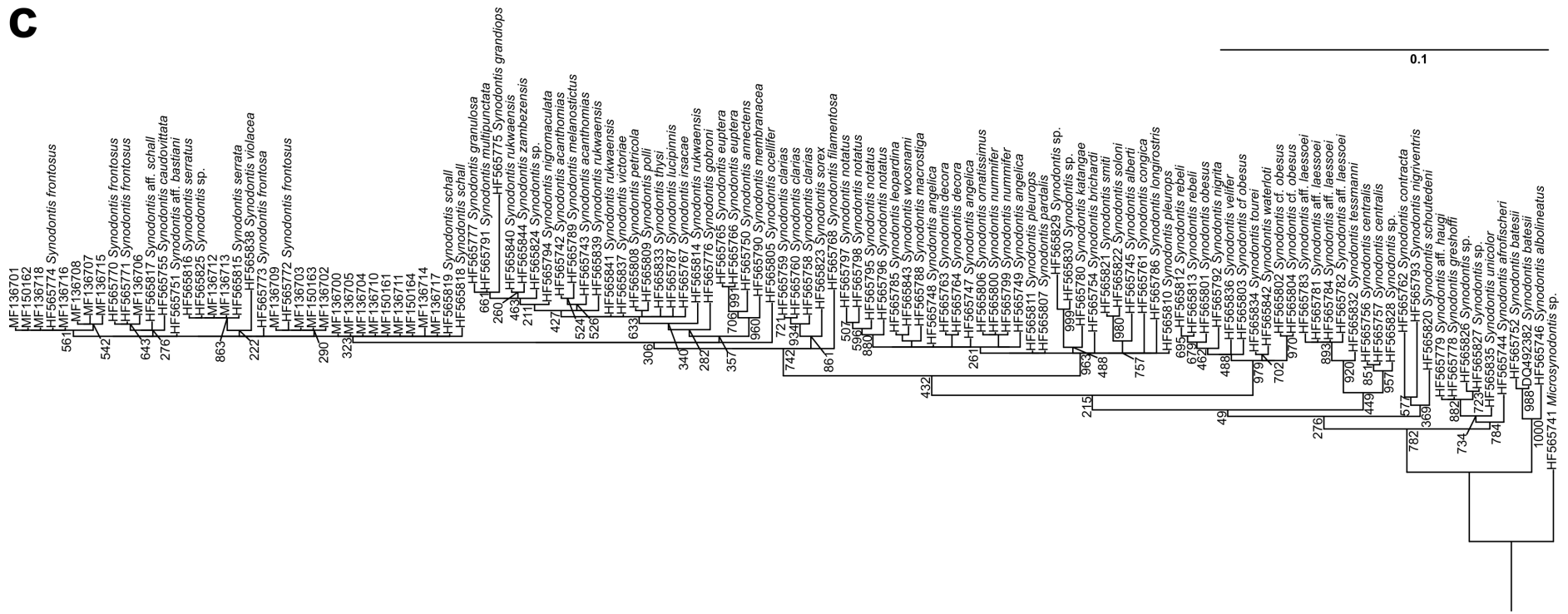


Figure S2. Phylogenetic trees for *coxI* a), *cytb* b) and *RAG2* c) as revealed by ML analyses, showing detailed branching with bootstraps as branch supports. Sequence data of *S. schall* Eastern clade obtained within the scope of this study are presented with GenBank numbers (see Tab. S2).

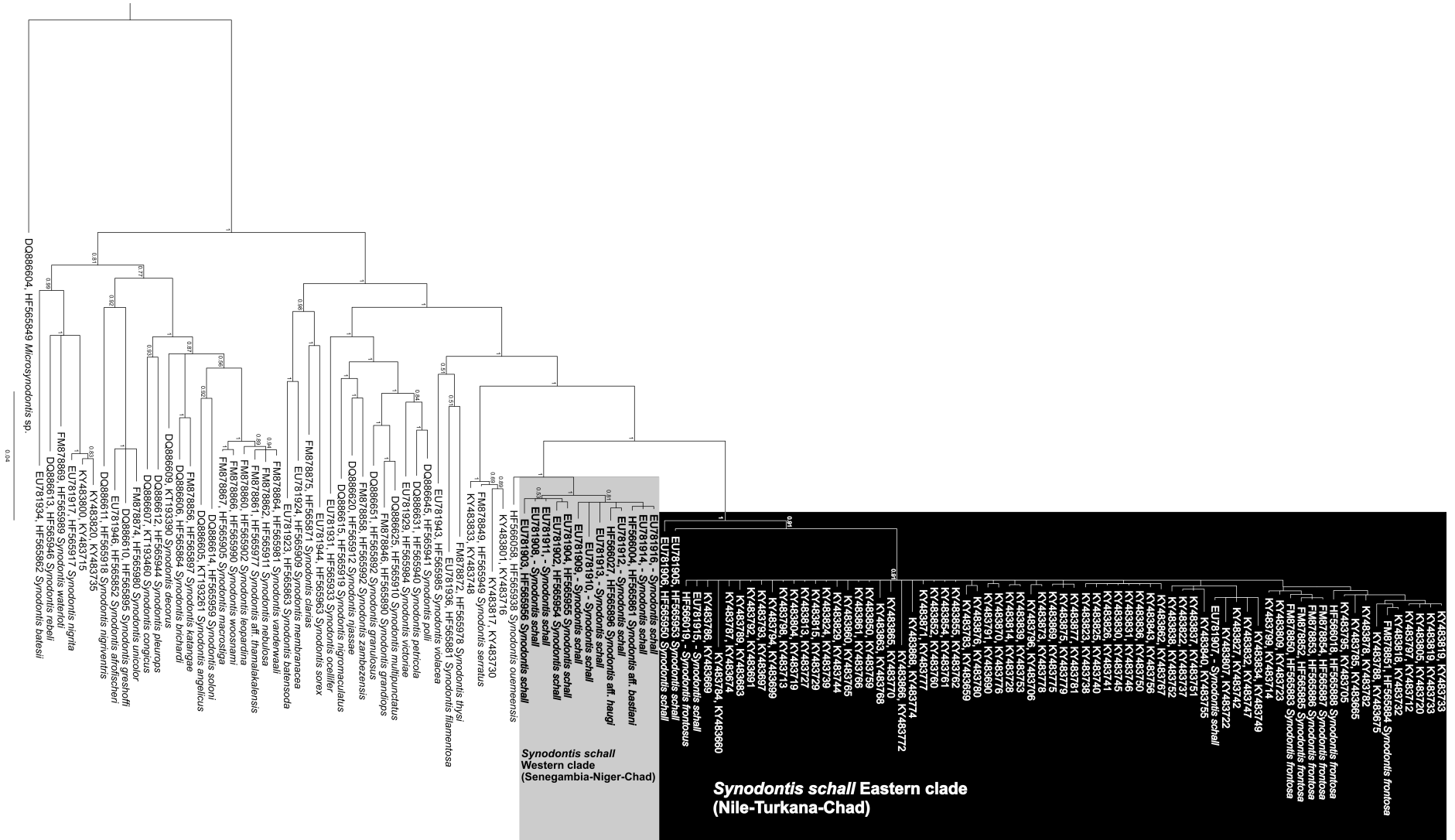


Figure S3. Phylogenetic analysis of concatenated dataset for mt genes (*cox1* and *cytb*) as revealed by BI analyses, showing detailed branching with posterior probabilities as branch supports. Final trees were created by software MrBayes. Sequence data of *S. schall* Eastern clade obtained within the scope of this study are presented with GenBank numbers. Data provided in separate file (see Tab. S1 and S2).

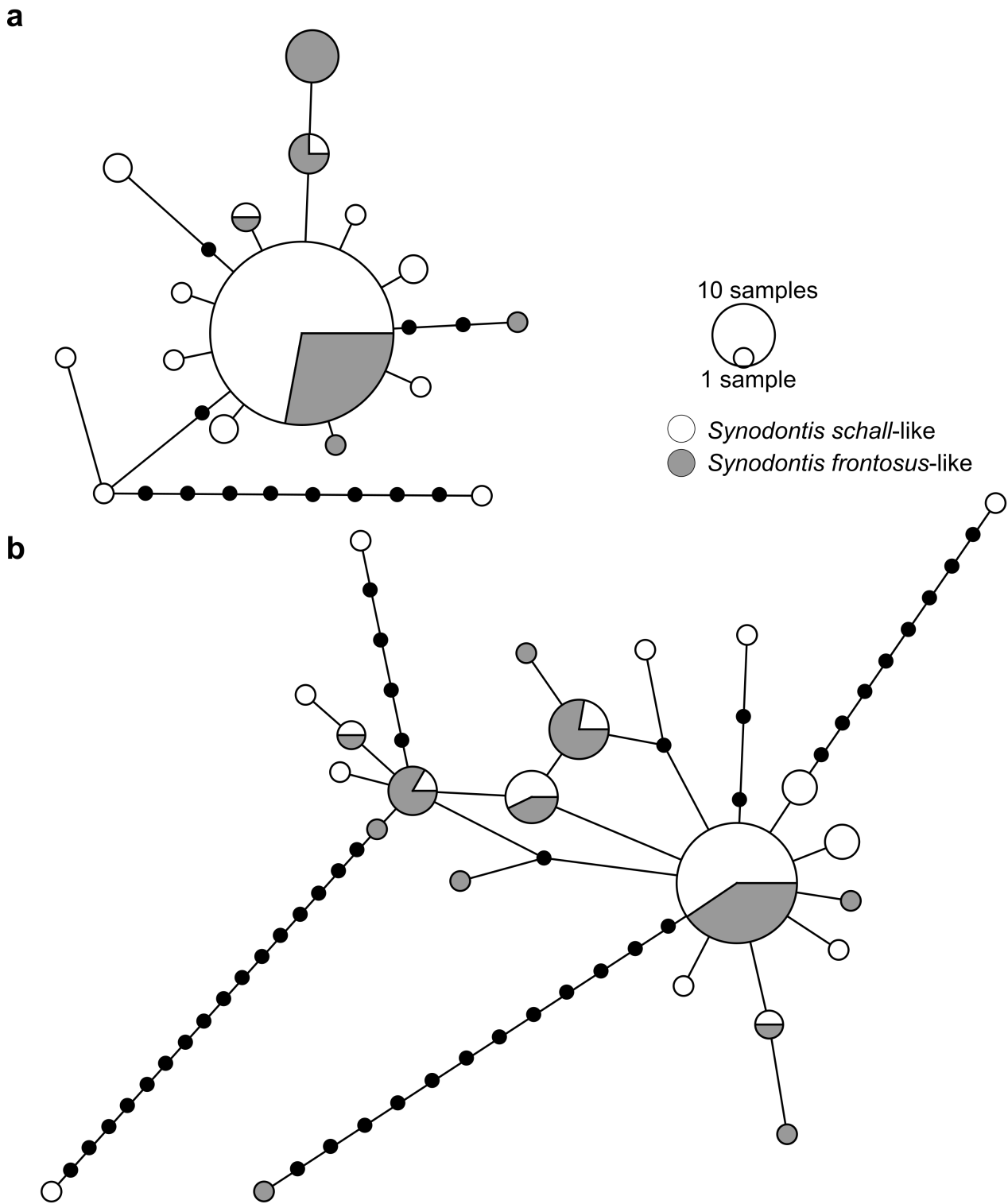


Figure S4. Haplotype networks for *coxI* (a) and *cytb* (b) constructed in software PopART v1.7. Networks were constructed only for samples obtained for this study. Sizes of haplo-nodes are relative to the sample size.